SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Lincoln, Steve
Klinger, Tod M.
Au-Young, Janice
Tang, Y. Tom
Goold, Richard
Akerblom, Ingrid E.
Seilhamer, Jeffrey J.
Hawkins, Phillip R.
Murry, Lynn E.
Delegeane, Angelo M.
Levine, Wendy B.
Hillman, Jennifer L.
Goli, Surya K.
Altus, Christina M.
Bandman, Olga
LaBrie, Samuel T.
Shah, Purvi

(ii) TITLE OF THE INVENTION: Database for Storage and Analysis of Full Length Sequences

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:
  (A) ADDRESSEE: Bozicevic & Reed, L.L.P.
  (B) STREET: 285 Hamilton Ave.
  (C) CITY: Palo Alto
  (D) STATE: CA
  (E) COUNTRY: U.S.
  (F) ZIP: 94301

(v) COMPUTER READABLE FORM:
  (A) MEDIUM TYPE: Diskette
  (B) COMPUTER: IBM Compatible
  (C) OPERATING SYSTEM: DOS
  (D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:
  (A) APPLICATION NUMBER: To Be Assigned
  (B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:
  (A) APPLICATION NUMBER: 08/282,955
  (B) FILING DATE: July 29, 1995

  (A) APPLICATION NUMBER: 08/187,530
  (B) FILING DATE: January 27, 1994

  (A) APPLICATION NUMBER: 08/179,873
  (B) FILING DATE: January 11, 1994

  (A) APPLICATION NUMBER: 08/100,523

　　　　(B) FILING DATE: August 3, 1993

　　　　(A) APPLICATION NUMBER: 07/977,780
　　　　(B) FILING DATE: November 19, 1992

5

　　　　(A) APPLICATION NUMBER: 07/916,491
　　　　(B) FILING DATE: July 17, 1992

　　　　(A) APPLICATION NUMBER: 08/289,822
10　　　(B) FILING DATE: August 12, 1994

　　　　(A) APPLICATION NUMBER: 08/581,240
　　　　(B) FILING DATE: December 29, 1995

15　　　(A) APPLICATION NUMBER: 08/657,697
　　　　(B) FILING DATE: May 29, 1996

　　　　(A) APPLICATION NUMBER: 08/747,547
　　　　(B) FILING DATE: November 12, 1996

20

　　　　(A) APPLICATION NUMBER: 08/712,710
　　　　(B) FILING DATE: September 12, 1996

　　　　(A) APPLICATION NUMBER: 08/744,026
25　　　(B) FILING DATE: November 5, 1996

　　　　(A) APPLICATION NUMBER: 08/786,999
　　　　(B) FILING DATE: January 23, 1997

30　　　(A) APPLICATION NUMBER: 08/822,262
　　　　(B) FILING DATE: March 20, 1997

　　　　(A) APPLICATION NUMBER: 08/000,000 (as yet unassigned)
　　　　(B) FILING DATE: October 16, 1997

35

　　(viii) ATTORNEY/AGENT INFORMATION:
　　　　(A) NAME: Francis, Carol L.
　　　　(B) REGISTRATION NUMBER: 36,513
　　　　(C) REFERENCE/DOCKET NUMBER: 6514/069001

40

　　(ix) TELECOMMUNICATION INFORMATION:
　　　　(A) TELEPHONE: 650-327-3400
　　　　(B) TELEFAX: 650-327-3231

45

　　　　(2) INFORMATION FOR SEQ ID NO:1:

　　(i) SEQUENCE CHARACTERISTICS:
　　　　(A) LENGTH: 373 base pairs
50　　　(B) TYPE: nucleic acid
　　　　(C) STRANDEDNESS: single
　　　　(D) TOPOLOGY: linear

　　(ii) MOLECULE TYPE: cDNA
55

　　(vii) IMMEDIATE SOURCE:
　　　　(A) LIBRARY: Pancreatic Cancer

48

(B) CLONE: PANC1A

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
5   GTACGGAGGT GAGGTTTGTN ACCGCGATTC TAAGAGGTGG GCTTTTAGTC CCTCCAGACC    60
    TCGGCTTTAG TGCTGTCTCC GCTTTTYTTT CACCTTCACA GAGGTTCGTG TCTTCCTAAA   120
    AGAAGGTTTT ATTGGGAGGT AAAGGTCAAT GCGTAGGGGT AGAGTAAGAT GTCTTATGGT   180
    GAAATTRAAG GTAAATTCTT GGGACCTAGA GAAGAAGTAA CGAGTGAGCC ACGCTGTAAA   240
    AAATTGAAGT CAACCACAGA GTCGTATGTT TTTCACAATC ATAGTAATGC TGATTTTCAC   300
10  AGNATCCAAG AGAAAACTGG AAATGATTGG GTCCCTGTGN NCATCATTGA TGTCAGAGGA   360
    CATAGTTATT TGC                                                     373
```

(2) INFORMATION FOR SEQ ID NO:2:

15

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 321 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
20   (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

  (vii) IMMEDIATE SOURCE:
25   (A) LIBRARY: Pancreatic Cancer
     (B) CLONE: PANC1B

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
30  GTGAGGTTTG TTACCNCGAT TCTGAGAGGT GGGCTTTTAG TCCCTCCAGA CCTCGGCTTT    60
    AGTGCTGTCT CCGMTTTTCT TTCACCTTCA CAGAGATGTC TTATGGTGAA ATTGAAGGTA   120
    AATTCTTGGG ACCTAGWGAA GAAGTAACGA GTGAGCCACG CTGTAAAAAA TTGAAGTCAA   180
    CCACAGAGTC GTATGTTTTT CACAATCATA GTAATGCTGA TTTTCACAGW ATCCAAGAGA   240
    AAACTGGAAA TGATTGGGT CCCTGTGACC ATCATTNATG TCAGAGGNCA TAGTTAATTT   300
35  GCAGGAGANC AAAAATCAAA A                                             321
```

(2) INFORMATION FOR SEQ ID NO:3:

   (i) SEQUENCE CHARACTERISTICS:
40   (A) LENGTH: 528 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

45   (ii) MOLECULE TYPE: cDNA

  (vii) IMMEDIATE SOURCE:
    (A) LIBRARY: NEUTGMT01
    (B) CLONE: 637393
50

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
    ATGACAGACT GTGAATTTGG ATATATTTAC AGGCTGGCTC AGGACTATCT GCAGTGCGTC    60
    CTACAGATAC CACAACCTGG ATCAGGTCCA AGCAAAACGT CCAGAGTGCT ACAAAATGTT   120
55  GCGTTCTCAG TCCAAAAAGA AGTGGAAAAG AATCTGAAGT CATGCTTGGA CAATGTTAAT   180
    GTTGTGTCCG TAGACACTGC CAGAACACTA TTCAACCAAG TGATGGAAAA GGAGTTTGAA   240
    GACGACATCA TTAACTGGGG AAGAATTGTA ACCATATTTG CATTTGAAGG TATTCTCATC   300
```

```
     AAGAAACTTC TACGACAGCA AATTGCCCCG GATGTGGATA CCTATAAGGA GATTTCATAT      360
     TTTGTTGCGG AGTTCATAAT GAATAACACA GGAGAATGGA TAAGGCAAAA CGGAGGCTGG      420
     GAAAATGGCT TTGTAAAGAA GTTTGAACCT AAATCTGGCT GGATGACTTT TCTAGAAGTT      480
     ACAGGAAAGA TCTGTGAAAT GCTATCTCTC CTGAAGCAAT ACTGTTGA                   528
```

5

(2) INFORMATION FOR SEQ ID NO:4:

10
      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 405 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

15   (ii) MOLECULE TYPE: cDNA

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
20  GTCCAAATCA CTCATTGTTT GTGAAAGCTG AGCTCACAGC AAAACAAGCC ACCATGAAGC      60
    TGTCGGTGTG TCTCCTGCTG GTCACGCTGG CCCTCTGCTG CTACCAGGCC AATGCCGAGT     120
    TCTGCCCAGC TCTTGTTTCT GAGCTGTTAG ACTTCTTCTT CATTAGTGAA CCTCTGTTCA     180
    AGTTAAGTCT TGCCAAATTT GATGCCCCTC CGGAAGCTGT TGCAGCCAAG TTAGGAGTGA     240
    AGAGATGCAC GGATCAGATG TCCCTTCAGA AACGAAGCCT CATTGCGGAA GTCCTGGTGA     300
25  AAATATTGAA GAAATGTAGT GTGTGACATG TAAAAACTTT CATCCTGGTT TCCACTGTCT     360
    TTCAATGACA CCCTGATCTT CACTGCAGAA TGTAAAGGTT TCAAC                     405
```


30 (2) INFORMATION FOR SEQ ID NO:5:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 495 base pairs
         (B) TYPE: nucleic acid
35   (C) STRANDEDNESS: double
         (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: cDNA

40   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
    GATCCTTGCC ACCCGCGACT GAACACCGAC AGCAGCAGCC TCACCATGAA GTTGCTGATG      60
    GTCCTCATGC TGGCGGCCCT CTCCCAGCAC TGCTACGCAG GCTCTGGCTG CCCCTTATTG     120
    GAGAATGTGA TTTCCAAGAC AATCAATCCA CAAGTGTCTA AGACTGAATA CAAAGAACTT     180
45  CTTCAAGAGT TCATAGACGA CAATGCCACT ACAAATGCCA TAGATGAATT GAAGGAATGT     240
    TTTCTTAACC AAACGGATGA AACTCTGAGC AATGTTGAGG TGTTTATGCA ATTAATATAT     300
    GACAGCAGTC TTTGTGATTT ATTTTAACTT TCTGCAAGAC CTTTGGCTCA CAGAACTGCA     360
    GGGTATGGTG AGAAACCAAC TACGGATTGC TGCAAACCAC ACCTTCTCTT TCTTATGTCT     420
    TTTTACTACA AACTACAAGA CAATTGTTGA AACCTGCTAT ACATGTTTAT TTTAATAAAT     480
50  TGATGGCAAA AACTG                                                      495
```


     (2) INFORMATION FOR SEQ ID NO:6:

55
      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 1143 base pairs
         (B) TYPE: nucleic acid

```
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: cDNA

    (vii) IMMEDIATE SOURCE:
        (A) LIBRARY:
        (B) CLONE: Consensus

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCCCCGCCG CGCCCGGCGC GCCCGCCGCC CGGGGGGATG TCTTACAAAC CGAACTTGGC    60
CGCGCACATG CCCGCCGCCG CCCTCAACGC CGCTGGGAGT GTCCACTCGC CTTCCACCAG   120
CATGGCAACG TCTTCACAGT ACCGCCAGCT GCTCAGTGAC TACGGGCCAC CGTCCCTAGG   180
CTACACCCAG GGAACTGGGA ACAGCCAGGT GCCCCAAAGC AAATACGCGG AGCTGCTGGC   240
CATCATTGAA GAGCTGGGGA AGGAGATCAG ACCCACGTAC GCAGGGAGCA AGAGTGCCAT   300
GGAGAGGCTG AAGCGCGGCA TCATTCACGC TAGAGGACTG GTTCGGGAGT TCTTGGCAGA   360
AACGGAACGG AATGCCAGAT CCTAGCTGCC TTGTTGGTTT TGAAGGATTT CCATCTTTTT   420
ACAAGATGAG AAGTTACAGT TCATCTCCCC TGTTCAGATG AAACCCTTGT TTTCAAAATG   480
GTTACAGTTT CGTTTTTCCT CCCATGGTTC ACTTGGCTCT GAACCTACAG TCTCAAAGAT   540
TGAGAAAAGA TTTTGCAGTT AATTAGGATT TGCATTTTAA GTAGTTAGGA ACTGCCCAGG   600
TTTTTTTTGT TTTTTAAGCA TTGATTTAAA AGATGCACGG AAAGTTATCT TACAGCAAAC   660
TGTAGTTTGC CTCCAAGACA CCATTGTCTC CCTTTAATCT TCTCTTTTGT ATACATTTGT   720
TACCCATGGT GTTCTTTGTT CCTTTTCATA AGCTAATACC ACTGTAGGGA TTTTGTTTTG   780
AACGCATATT GACAGCACGC TTTACTTAGT AGCCGGTTCC CATTTGCCAT ACAATGTAGG   840
TTCTGCTTAA TGTAACTTCT TTTTTGCTTA AGCATTTGCA TGACTATTAG TGCTTCAAAG   900
TCAATTTTTA AAAATGCACA AGTTATAAAT ACAGAAGAAA GAGCAACCCA CCAAACCTAA   960
CAAGGACCCC CGAACACTTT CATACTAAGA CTGTAAGTAG ATCTCAGTTC TGCGTTTATT  1020
GTAAGTTGAT AAAAACATCT GGAAGAAAAT GACTAAAACT GTTTGCATCT TTGTATGTAT  1080
TTATTACTTG ATGTAATAAA GCTTATTTTC ATAACAATT TGTATTAAAA TGTGGGTTCC  1140
TTG                                                               1143


    (2) INFORMATION FOR SEQ ID NO:7:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 871 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
        (A) LIBRARY:
        (B) CLONE: Consensus

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACCTGCTGGC CCCTGGACAC CTCTGTCACC ATGTGGTTCC TGGTTCTGTG CCTCGCCCTG    60
TCCCTGGGGG GGACTGGTGC TGCGCCCCCG ATTCAGTCCC GGATTGTGGG AGGCTGGGAG   120
TGTGAGCAGC ATTCCCAGCC CTGGCAGGCG GCACTGGTCA TGGAAAACGA ATTGTTCTGC   180
TCGGGCGTCC TGGTGCATCC GCAGTGGGTG CTGTCAGCCG CACACTGTTT CCAGAACTCC   240
TACACCATCG GGCTGGGCCT GCACAGTCTT GAGGCCGACC AAGAGCCAGG GAGCCAGATG   300
GTGGAGGCCA GCCTCTCCGT ACGGCACCCA GAGTACAACA GACCCTTGCT CGCTAACGAC   360
CTCATGNTCA TCAAGTTGGA CGAATCCGTG TCCGAGTCTG ACAACATCCG GAGNATCAGC   420
ATTGNTTCGC AGTGCCCTAC CGCGGGGAAC TTTTGCCTCG TTTCTGGCTG GGGTCTGCTG   480
```

51

```
    GCGAACGGCA GAATGCCTAC CGTGCTGCAG TGCGTGAACG TGTCGGTGGT GTCTGAGGAG       540
    GTCTGCAGTA AGCTCTATGA CCCGCTGTAC CACCCCAGCA TGTTCTGCGC CGGCGGAGGG       600
    CAAGACCAGA AGGACTCCTG CAACGGTGAC TCTGGGGGGC CCCTGATCTG CAACGGGTAC       660
    TTGCAGGGCC TTGTGTCTTT CGGAAAAGCC CCGTGTGGCC AAGTTGGCGT GCCAGGTGTC       720
  5 TACACCAACC TCTGCAAATT CACTGAGTGG ATAGAGAAAA CCGTCCAGGC CAGTTAACTC       780
    TGGGGACTGG GAACCCATGA AATTGACCCC CAAATACATC CTGCGGAAGG AATTCAGGAA       840
    TATCTGTTCC CAGCCCCTCC TCCCTCAGGC C                                     871
```

10   (2) INFORMATION FOR SEQ ID NO:8:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 1428 base pairs
                (B) TYPE: nucleic acid
15   (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

            (vii) IMMEDIATE SOURCE:
                (A) LIBRARY: Colnnot01
20   (B) CLONE: 609476

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
    GGCCGGGTTG GGGGTGTGCG ATTGTGTGGG ACGGTCTGGG GCAGCCCAGC AGCGGCTGAC        60
 25 CCTCTGCCTG CGGGGAAGGG AGTCGCCAGG CGGCCGTCAT GGCGGTGTCG GAGAGCCAGC       120
    TCAAGAAAAT GGTGTCCAAG TACAAATACA GAGACCTAAC TGTACGTGAA ACTGTCAATG       180
    TTATTACTCT ATACAAAGAT CTCAAACCTG TTTTGGATTC ATATGTTTTT AACGATGGCA       240
    GTTCCAGGGA ACTAATGAAC CTCACTGGAA CAATCCCTGT GCCTTATAGA GGTAATACAT       300
    ACAATATTCC AAATATGCCTA TGGCTACTGG ACACATACCC ATATAATCCC CCTATCTGTT       360
 30 TTGTTAAGCC TACTAGTTCA ATGACTATTA AAACAGGAAA GCATGTTGAT GCAAATGGGA       420
    AGATATATCT TCCTTATCTA CATGAATGGA AACACCCACA GTCAGACTTG TTGGGGCTTA       480
    TTCAGGTCAT GATTGTGGTA TTTGGAGATG AACCTCCAGT CTTCTCTCGT CCTATTTCGG       540
    CATCCTATCC GCCATACCAG GCAACGGGGC CACCAAATAC TTCCTACATG CCAGGCATGC       600
    CAGGTGGAAT CTCTCCATAC CCATCCGGAT ACCCTCCCAA TCCCAGTGGT TACCCAGGCT       660
 35 GTCCTTACCC ACCTGGTGGT CCATATCCTG CCACAACAAG TTCTCAGTAC CCTTCTCAGC       720
    CTCCTGTGAC CACTGTTGGT CCCAGTAGGG ATGGCACAAT CAGCGAGGAC ACCATCCGAG       780
    CCTCTCTCAT CTCTGCGGTC AGTGACAAAC TGAGATGGCG GATGAAGGAG GAAATGGATC       840
    GTGCCCAGGC AGAGCTCAAT GCCTTGAAAC GAACAGAAGA AGACCTGAAA AAGGGTCACC       900
    AGAAACTGGA AGAGATGGTT ACCCGTTTAG ATCAAGAAGT AGCCGAGGTT GATAAAAACA       960
 40 TAGAACTTTT GAAAAAGAAG GATGAAGAAC TCAGTTCTGC TCTGGAAAAA ATGGAAAATC      1020
    AGTCTGAAAA CAATGATATC GATGAAGTTA TCATTCCCAC AGCTCCCTTA TACAAACAGA      1080
    TCCTGAATCT GTATGCAGAA GAAACGCTA TTGAAGACAC TATCTTTTAC TTGGGAGAAG      1140
    CCTTGAGAAG GGGCGTGATA GACCTGGATG TCTTCCTGAA GCATGTACGT CTTCTGTCCC      1200
    GTAAACAGTT CCAGCTGAGG GCACTAATGC AAAAAGCAAG AAAGACTGCC GGTCTCAGTG      1260
 45 ACCTCTACTG ACTTCTCTGA TACCAGCTGG AGGTTGAGCT CTTCTTAAAG TATTCTTCTC      1320
    TTCCTTTTAT CAGTAGGTGC CCAGAATAAG TTATTGCAGT TTATCATTCA MGTGTAAAAT      1380
    ATTTGAATC AATAATATAT TTTCTGTTTT CTTTTGGTAA AGATGGAT                  1428
```

            (2) INFORMATION FOR SEQ ID NO:9:
50
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 667 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
55   (D) TOPOLOGY: linear

            (vii) IMMEDIATE SOURCE:

```
       (A) LIBRARY: THP1NOTO3
       (B) CLONE: 2446131

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
  5
   GGCTGAGCGG CCCCGCAGCC AACCCCCGAG GAGCGGCCGG CTGGCGTCCG CCGCGCCCAG    60
   GAGTTGGGGA TGTCCTACAA ACCCATCGCC CCTGCTCCCA GCAKCACCCC TGGCTCCAGC   120
   ACCCCTGGGC CGGGCACCCC GGTCCCTACA GGAAGCGTCC CGTCGCCGTC GGGCTCAGTG   180
   CCAGGAGCCG GCGCTCCTTT CAGACCGCTG TTTAACGACT TTGGACCGCC TTCCATGGGC   240
 10 TACGTGCAGG CGATGAAGCC ACCCGGCGCC CAGGGCTCCC AGAGCACCTA CACGGACCTG   300
   CTGTCAGTCA TAGAGGAGAT GGGCAAAGAG ATCCGGCCTA CCTATGCTGG CAGCAAGAGC   360
   GCCATGGAGC GCCTGAAGAG AGGTATCATC CATGCCCGGG CCCTAGTCAG AGAGTGCCTG   420
   GCAGAGACAG AGCGGAACGC CCGCACGTAA CAGGAAGCGC CTCGGCCTCA GCGTCTGGAC   480
   CTATCCGGCC ACTGCAGAGC ACCCGCTTCT CCCTGGCCTT CATCCCGAGT TGCACTAACC   540
 15 ATCCTGGGCT TCCTGTCCTG TGTCCCTTGG TGGGTCCCCT CCAGGAACCA AGGAGTGGCC   600
   CTCCAGGTGG CAGCACTAAG GACACCCCCC CACAACAAGA GTTAGCAGCG AGGTCCCCAT   660
   GAGTCCC                                                            667


             (2) INFORMATION FOR SEQ ID NO:10: -
 20
       (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 397 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: single
 25      (D) TOPOLOGY: linear


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

 30 CTGAACTCTA CCTGGTGACC AGGGACCAGG ACCTTTATAA GGTGGAAGGC TTGATGTCCT    60
   CCCCAGACTC AGCTCCTGGT GAAGCTCCCA GCCATCAGCC ATGAGGGTCT TGTATCTCCT   120
   CTTCTCGTTC CTCTTCATAT TCCTGATGCC TCTTCCAGGT GTTTTTGGTG GTATAGGCGA   180
   TCCCGTTACC TGCCTTAAGA GTGGAGCCAT ATGTCATCCA GTCTTTTGCC CTAGAAGGTA   240
   TAAACNAATT GGCACCTGTG GTCTCCCTGG AACAAATGC TGNAAAAAGC CATGAGGAGG    300
 35 CCAAGAAGCT GCTGTGGCNG ANGCGGATTC AGAAAGGGCT CCCTCATCAG AGANGTGCGA   360
   CATGTAAACC AAATTAAACT ATGGTGTCCA ANGATAN                           397
```